



Docket No.: UTSD:1276USC1

Serial No.: 09/686,346

Inventor(s): Cobb et al.

Title: "TAO Protein Kinase Polypeptides and Methods of Use Thereof"

1 TCTGCAGTATGGTAGATTATTATTTATGCATTATGCCAGTGTGGCTTCATTACACAGATGAACCAAGCTTTGGGATAGCAGTATAAAATTAGAATCAGACAGCTGACTGCTC
115 AGCAGGATGCCATCAACTAACAGAGCAGGAGTCTAAAGGACCCGAAATCGCAGAGCTCTCTTCAAGAAGATCCGGAAGAACTCTTCACAGATCTCAGAGAAATCGGCCAT
M P S T N R A G S L K D P E I A E L F F K E D P E K L F T D L R E I G H 36

229 GGGAGCTTTGGAGCAGTTTATTTGCACGAGATGTGCTACTAATGAAGTGGTGGCCATCAAGAAAATGCTTATAGTGAAGCAGTCTACTGAGAAATGGCAGGATATTATT
G S F G A V Y F A R D V R T N E V V A I K K M S Y S G K Q S T E K W Q D I I 74

343 AAGGAAGTCAAGTTTCTACAAAGAATAAAACATCCCAACAGTATAGATACAAGGCTGCTATTTACGTGAACACACAGCATGGCTTGAATGGAATATTGTTAGGATCTGCT
K E V K F L Q R I K H P N S I E Y K G C Y L R E H T A W L V M E Y C L G S A 112

457 TCGATTACTAGAGTTTCAAAAAGCCATTACAAGAGTGAATAGCAGCAATTACACATGGTCTCTCCAGGATTAGCTTATTACATTCTCATACCATGATCCATAGA
S D L L E V H K K P L Q E V E I A A I T H G A L O G L A Y L H S H T M I H R 150

571 GATATCAAGCAGGAAATATCCTTCTGACAGAACAGGCCAAGTGAACCTTGCTGACTTTGGATCTGCTCCATGGCTCCCTGCCAATCTTTTGTGGGAACCATATTGG
D I K A G N I L L T E P G Q V K L A D F G S A S M A S P A N S F V G T P Y W 188

685 ATGGCCCCAGAAGTAATTTTAGCCATGGATGAAGGCAATATGATGGCAAGTGTATGCTCTTGAATAACATGATTGAATTAGCCGAGAGGAGGCCCTCTTTATTT
M A P E V I L A M D E G Q Y D G K V D V W S L G I T C I E L A E R K P P L F 226

799 AATATGAATGCAATGAGTGCCTTATATACATAGCCCAAAATGAATCCCTACACTACAGTCTAATGAATGGTCTGATTATTTTGAACCTTTGTAGATTCTTGCTCCAGAAA
N M N A M S A L Y H I A Q N E S P T L Q S N E W S D Y F R N F V D S C L Q K 264

913 ATCCCTCAAGATCGCCCTACATCAGAGGAACCTTTTAAAGCAGTGTGTTCTTCGAGAGGCCCTGAAACAGTGTTAATAGATCTTATTCAAGGACAAGGATGCAGTAAGA
I P Q D R P T S E E L L K H M F V L R E R P E T V L I D L I Q R T K D A V R 302

1027 GAGCTGGACAATCTACAATATCGAAAGATGAAGAACTCTTTTCCAGAGGCACATAATGGACCAGCAGTAGAAGCAGGAAAGAGGAGGAGCAAGATCATGGTGGTGGC
E L D N L Q Y R K M K K L L F Q E A H N G P A V E A Q E E E E E Q D H G G G 340

1141 CGACAGGAACAGTAAATAGTGTGGAAGCAATCAGTCTATCCCAGTATGTCTATCAGTGGCAGTAGCCAAAGCAGCAGTGTTAATAGTCTTCCAGATGCATCGGATGACAAG
R T G T V N S V G S N Q S I P S M S I S A S S Q S S S V N S L P D A S D D K 378

1255 AGTGAGCTAGACATGATGAGGGAGACCATACAGTGTCTAAGCAGTCTGTCTATCCACTTAAACCTGAGGAGGAAAAATTACCAAGAAGAGGAGATCTTAGAACAGAGCA
S E L D M M E G D H T V M S N S S V I H L K P E E E N Y Q E E G D P R T R A 416

1368 TCAGTCCACAGTCTCCACCTCAAGTGTCTGTCACAAATCATTATCGTAATAGAGAACACTTTGCAACTATACGAACAGCATCACTGGTTACAAGACAGATGCAAGAACAT
S A P Q S P P Q V S R H K S H Y R N R E H F A T I R T A S L V T R Q M Q E H 454

1483 GAGCAGGACTCTGAACCTAGAGAACAGATGTCTGTTATAAGCGGATGAGGCGACAGCATCAGAAGCAGCTGATGACTCTGGAATAAATGAAGGCAAGAAATGGACGAACAT
E Q D S E L R E Q M S G Y K R M R R Q H Q K Q L M T L E N K L K A E M D E H 492

1597 CGGCTCAGATTAGACAAAGATCTTGAACCTCAGCGCAACAAATTCGTCGAGAAATGGAGAACTTATTAAGAAACCAAGCTTCTATGAAAAAGAGGCTAAAGTATGGCC
R L R L D K D L E T O R N N F A A E M E K L I K K H O A S M E K E A K V M A 530

FIG. 1



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1711 AACGAGGAGAAAAAATCCAACAACATTCAAGCTCAACAGAGAAGAACTGAATAGCTTTTGGAGTCTCAAAAAGAGAATATAAATTCGAAAAGAGCAGCTTAAGGAG
N E E K K F Q Q H I Q A Q Q K K E L N S F L E S Q K R E Y K L R K E Q L K E 568

1825 GAGCTGAATGAAAAACAGAGCACACCTAAAAAGAAAAGCAGGAATGGCTTTCAAGCAGAAGGAGAATTTCAACATTTTCAGGCAGAAGAAGCTAATCTTTCGACGT
E L N E N Q S T P K K E K Q E W L S K O K E N I O H F Q A E E E A N L L R R 606

1939 CAAAGGAGTATCTAGAGTAGAATGTCGTGCTTCAAAAGAAGATGTTACTTGGTCGGCATAACTTGAACAGGACCTTGTGAGGAGGAGTTAAACAAAAGGCAGACTCAG
Q R Q Y L E L E C R R F K R R M L L G R H N L E Q D L V R E E L N K R Q T O 644

2053 AAGGACTTAGAACATGCAATGTTACTGCGACAGCATGAATCCATGCAAGAACTGGAGTTTCGCCACCTCAACACTATTGAGAAGATGCGCTGTGAGTTGATCAGACTGCAACAT
K D L E H A M L L R Q H E S M Q E L E F R H L N T I Q K M R C E L I R L Q H 682

2167 CAACTGAGCTTACTAACCAGCTGGAATACAATAAGAGAAGGGAACGGAACTAAGACGGAACATGTGATGGAAGTTTCAGACAGCAGCTTAAGAGTTTGAAGTCTAAAGAACTC
Q T E L T N Q L E Y N K R R E R E L R R K H V M E V R Q Q P K S L K S K E L 720

2281 CAAATAAAAAAGCAGTTTCAGGATACCTGCAAAATTCAAACAGACAGTACAAAGCATTAAAGGAATCACCTACTGGAGACTACACCAAGAGTGAGCACAAGCTGTTCTGAAA
Q I K K Q F O D T C K I Q T R Q Y K A L R N H L L E T T P K S E H K A V L K 758

2395 AGACTCAAGGAGGAACAGACTCGAAGTTAGCCATCTTGGCTGAGCAGTATGATCATAGCATTAAATGAATGCTCTCCACACAAGCTCTGCGTTTGGATGAAGCACAGGAAGCA
R L K E E Q T R K L A I L A E Q Y D H S I N E M L S T Q A L R L D E A O E A 796

2509 GAATGCCAGGTTTTGAAGATGCAGCTACAGCAGGAAGTGAAGCTGTTGAATGCATATCAGAGCAAAATCAAGATGCAGGCTGAGGCCAACATGATCGAGAGCTTCGAGAGCTG
E C Q V L K M Q L Q Q E L E L L N A Y Q S K I K M Q A E A Q H D R E L R E L 834

2623 GAACAAAGGGTCTCCCTTCGGAGAGCACTTTAGAACAGAAGATTGAAGAGAGATGTTGGCTTTGCAGATGAACGCACAGAACGAATACGTAGCCTGCTCGAGGCCAGGCC
E Q R V S L R R A L L E Q K I E E E M L A L Q N E R T E R I R S L L E R O A 872

2737 AGAGAAATTGAAGCTTTTGAAGCTGTAAGCATGAGATTAGGTTTTAGTAACATGGTCTTTCTAATCTCTCCCTGAGGCATTGAGCCACAGCTACCCAGGAGCTTCTAGCTGG
R E I E A F D S E S M R L G F S N M V L S N L S P E A F S H S Y P G A S S W 910

2851 TCTCACAATCCTACTGGGGTTCAAGCAGCTCACTGGGTCATCCATGGGTGGCACACCACAAGCTTGGGTCATCCGATGCAAGGCGGACCCCAACCATGGGGTCAACCCCTCA
S H N P T G G S G P H W G H P M G G T P Q A W G H P M Q G G P Q P W G H P S 948

2965 GGGCAATGCAAGGGGTACCTCGAGTAGCAGTATAGGAGTCCGCAATAGCCCCAGGCTCTGAGGGGACAGCTTCTGGGGACGGACGGAACAGGGCATGAGCAGAGCAGC
G P M Q G V P R G S S I G V R N S P Q A L R R T A S G G R T E Q G M S R S T 986

3079 AGTGTCACTTCACAAATATCCAATGGGTACACATGTCTTACACATAATAATTGAAAGTGGAATTCGCTGGAGCTGTGCTGCAAAAAGAACTGCCTACAGACATCAGCAGAC
S V T S Q I S N G S H M S Y T * * 1001

3193 CAGCCTCCTCACTTGGGTACTACCGGGTGAAGCTGTGCATATGGTATATTTTATTCGTCTTTGTAAGCGTTATGTTTGTGTTTACTAATTGGGATGTCATAGTATTTGGCTG

FIG.1 Cont.



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	I	II	III					
TA01	MPSTNRAGSLKOP	EIAELFFKEDPEKLF	TDLREIGHGSGF	GAFFARDVRTNEVVAIKMMSYSGKQSTKW--QDI	KEV 77			
TA02	MPAGGRAGSLKOP	DAELFFKDDPEKLF	SDLREIGHGSGF	GAFFARDVRNSEVVAIKMMSYSGKQSNKEW--QDI	KEV 77			
ceTOA	-MAPAVLQKPGV	IKDPSTIAALF	SNKQPEQDLREIGHGSGF	GAFFAYDKKNEQTVAIKMMNFGKQAVEKW--NDI	KEV 76			
STE20	REERERRKKQLY	AKLNEICSDGDP	STKYANLVKIGGAS	GGVYTAYEIGTNVSVAIKQMNLE-KQPKKELI	INEILVWK 670			
	IV	V	VI					
TA01	KFLQRIKHPNS	IEYKGCYLREHTA	WLVMEYCLGSAS	DLLEVHKKPLQVE	ETAAITHGALQGLAYLHSHITMIHRDI	KAGN 156		
TA02	RFLOKLHPNT	IQYRGCVLREHTA	WLVMEYCLGSASE	FLVHKKPLQVE	ETAAVTHGALQGLAYLHSHINMIHRD	VKAGN 156		
ceTOA	SFLNTVHPH	IVDYKACFLKDT	TCLWLVMEYCLGSAA	DIVDLRKGMR	VEETAAICSQTLDA	RLYLSLKR	IHRDI	KAGN 155
STE20	G----	SKHPNIVNFID	SYVLKGLWVIMEY	MEGFS	LDV-VTHCILTEGQ	ICAVCRETLSGLE	FLHSGVLRD	IKSDN 744
	VII	VIII	IX					
TA01	ILLTEPGQVKL	ADFGSAS----	MASPANSFVGTPY	WMAPEVILAMDE	GQYDGKVDVWS	IGITCIELAER	KPPLFMNA	230
TA02	ILLSEPGLVKL	ADFGSAS----	IMAPANSFVGTPY	WMAPEVILAMDE	GQYDGKVDVWS	IGITCIELADR	KPPLFMNA	230
ceTOA	ILLSOHAIVKL	ADFGSAS----	LVDPAQTFIGT	PFMAPEVILAMDE	GHYTDRA	DVWSIGITCIELAER	KPPLFSMA	229
STE20	ILLSMEGDIKL	TDGFCQAQINEL	NLKRRTTWGTPY	WMAPEV	SRKE---YGP	KVDVWSIGITCIELA	EMIEGEPY	LNETP 819
	X	XI						
TA01	MSALYHTAQNE	SPTLQSN	EWSDYFRN-----	FVDSCLQKIPQDR	PTSE 273			
TA02	MSALYHTAQNE	SPTLQSN	EWSDYFRN-----	FVDSCLQKIPQDR	PTSE 273			
ceTOA	MSALYHTAQND	PPTLS	PIDTSEQPEWSLE	FVQFIDKCLRKPAE	ERMSAE 279			
STE20	LRALYLIATN	CTPKLKEPEN	LSS-----SLKK--	FLDWCLC	VEPEDRASAT 863			

FIG.2



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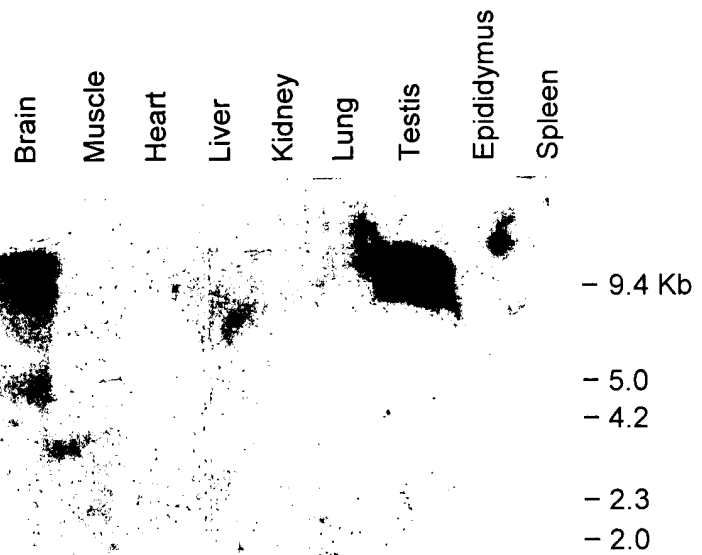


FIG.3A

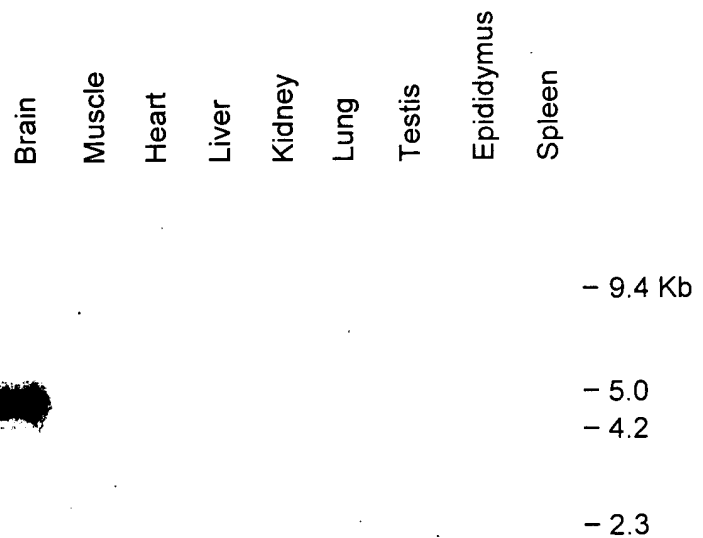


FIG.3B



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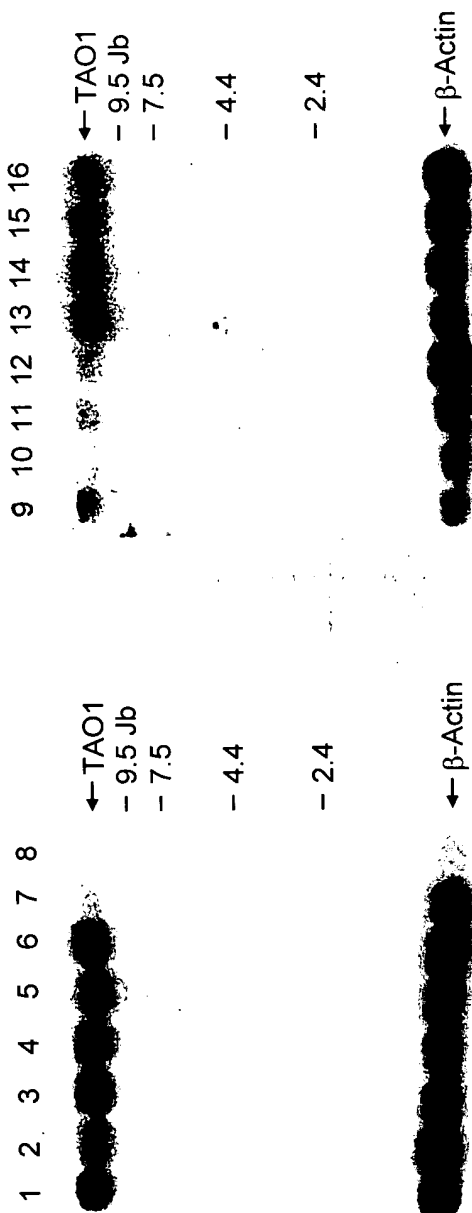


FIG.4B

FIG.4A



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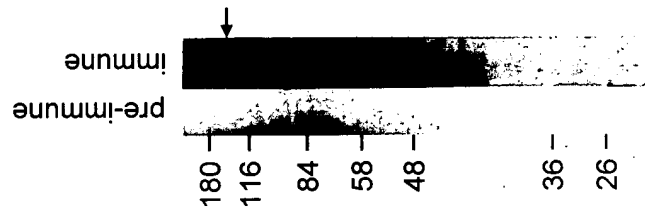


FIG. 5C

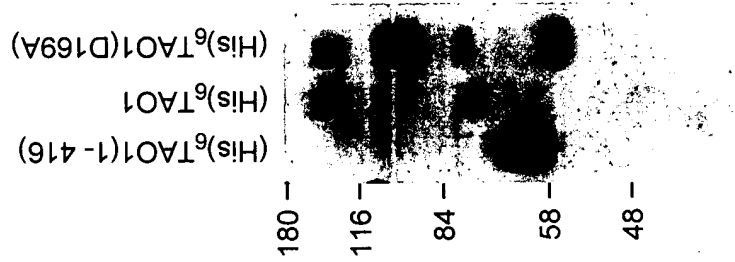


FIG. 5B

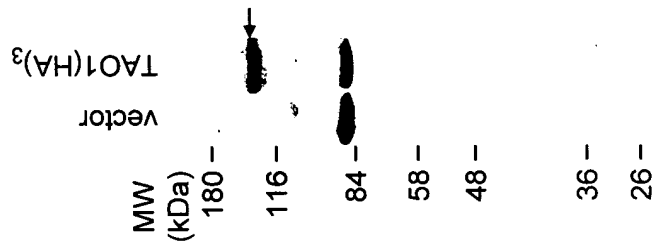


FIG. 5A



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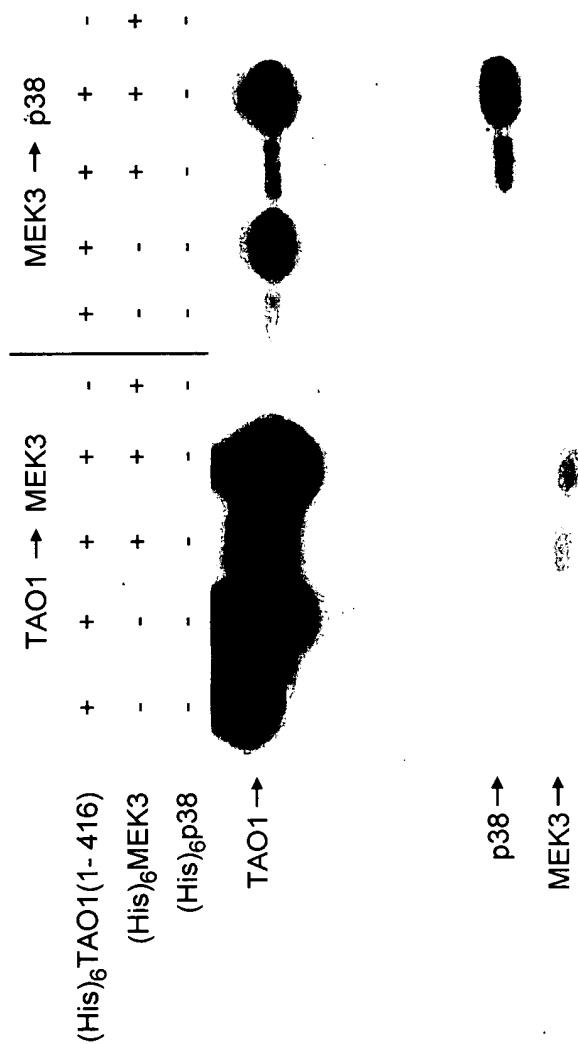


FIG.6



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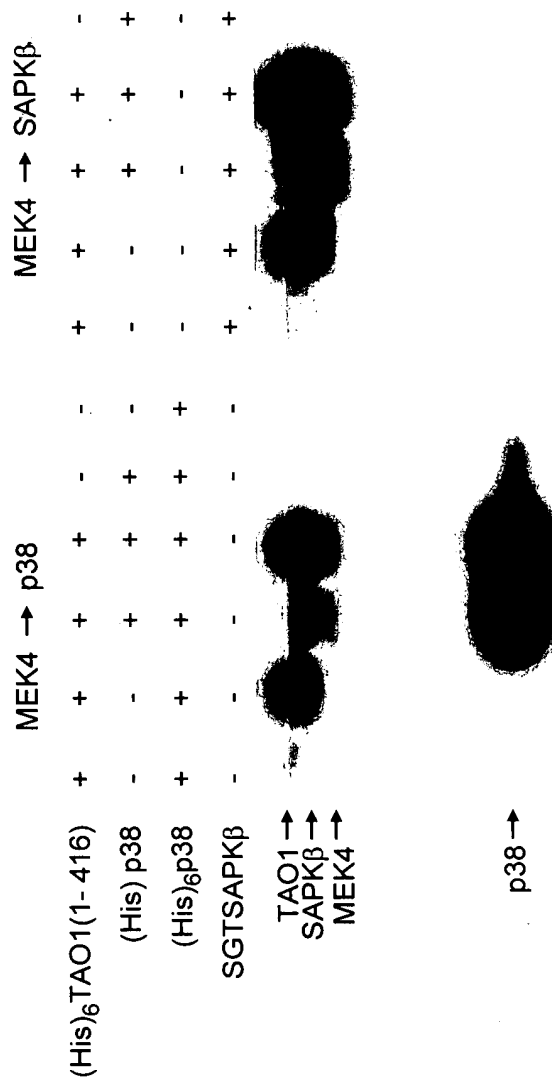


FIG.7



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	MEK6 → p38			
(His) ₆ TAQ1(1- 416)	+	+	-	-
GSTMEK6	-	+	+	-
(His) ₆ p38	+	+	+	+

TAO1 →



MEK6 →

p38 →



FIG.8



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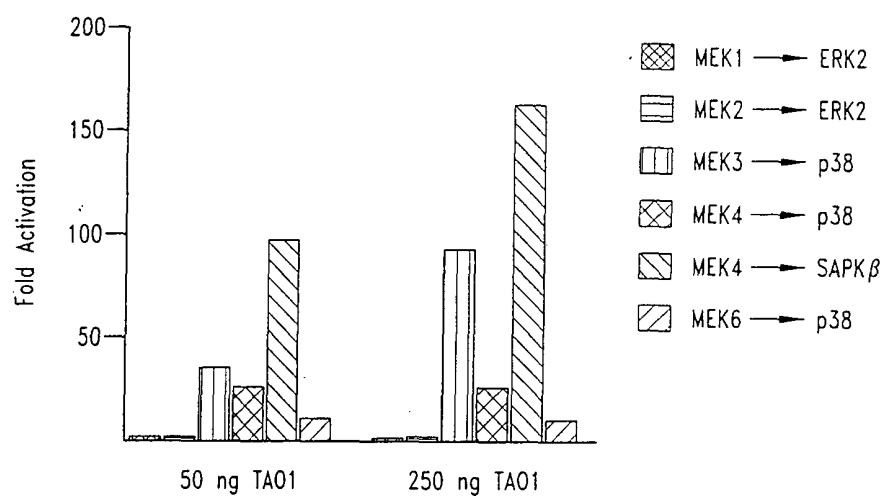


FIG.9



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vector	+	+	-	-
pCMV5TAO1(HA) ₃	-	-	+	+
pCMV5mycMEK3	-	+	+	+



FIG.10



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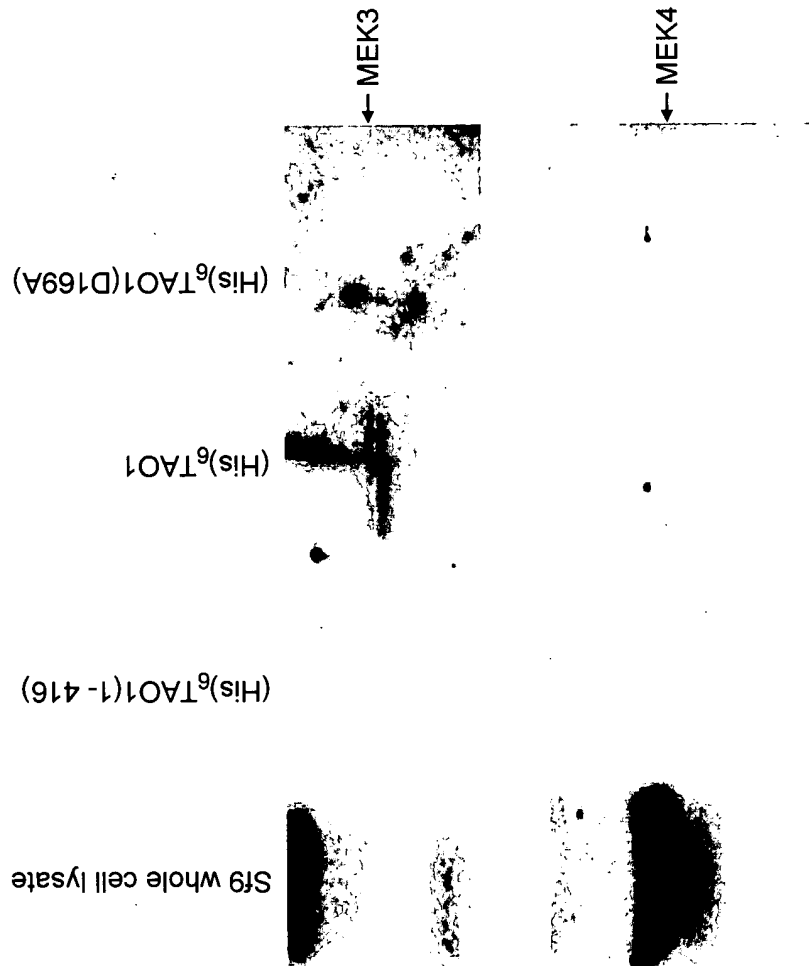


FIG. 11

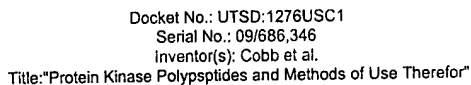


FIG. 12



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Query: 964 GAACAAACATGTGCTTTAAAAGTTCCTCTGATGTAGGGCGATCTTGAGGGATTTTCTGGA 905
      ||||| ||| |||| |||| ||||| || | |||| ||||| |||
Sbjct: 79 GAACAAAGTCATGCCCTTAATAGTTCTGCTGATGTTGGCTTTCTGAGGTATTTCTGCA 138

Query: 904 GGCAAGAATCTACAAAGTTTCGAAAATAATCAGACCATTATTAGACTGTAGTGTAGGG 845
      ||| |||| |||| | ||| | || ||||| ||||| || |||
Sbjct: 139 AGCAGTAATCAACAAATCTCCTAAAGGAGTCTGTCCATTATTAGACTGTAACGTTGGG 198

Query: 844 ATTCATTTGGGCTATGTGATATAAGGCACTATTGCATTATTAATAAAGGAGGCT 785
      | |||| |||| ||||| ||||| ||||| ||||| || || | || |||
Sbjct: 199 AGTCATTCTGGCAATGTGATATAAGGCACTATTGCATTATGTTGAAAAGGGCGGCT 258

Query: 784 TCCTCTCGGCTAATTCAATACATGTTATTCCAAGAGACCATACATCAACTTGGCCATCAT 725
      ||| || || ||||| |||| || || |||| |||| | ||||| |||||
Sbjct: 259 TCCGTTCCGCCAATTCAATACAAGTGATGCCAAGTGACCAATATCAACTTCCCATCAT 318

Query: 724 ATTGTCCTTCATCCATGGCTAAAATTACTTCTGGGGCCATCCAATATGGTGTCCACAA 665
      | ||||| ||||| |||| || || |||| ||||| || |||| |||| |
Sbjct: 319 ACTGTCCTTCATCCATAGCTAAGATCACCTCTGGAGCCATCCAGTAAGGTGTGCCACGA 378

Query: 664 AAGAATTGGCAGG 651
      || |||| ||
Sbjct: 379 AGGAGTTGGCCAGG 392
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FIG.13

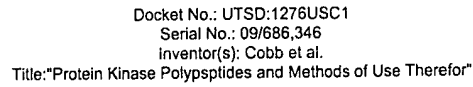


FIG. 14

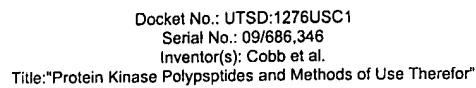
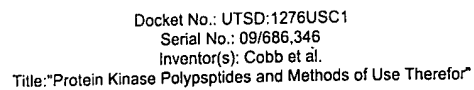


FIG. 15A

FIG. 15B





Query: 3228 GTGCATATGGTATATTTTATTCGTCTTTGTAAAGCGTTATGTTTTGTGTTTACTAATTGG 3287
|||||
Sbjct: 31 GTGCATATGGTATATTTNATTCATTTTGTAAAGCGTTCGTGTTTGTGTTTACTAATTGG 90

Query: 3288 GATGTCATAGTATTTGGCTGCCGGG 3312
|||||
Sbjct: 91 GATGTCATAGTACTTGGCTGCCGGG 115

FIG.17A

Query: 3200 CTCACCTGGGTACTACCGGGTGAAGCTGTGCATATGGTATATTT 3245
|||||
Sbjct: 1 CTCACCTGGGTACTACAGTGTGAAGCTGAGTGCATATGGTATATT 46

FIG.17B

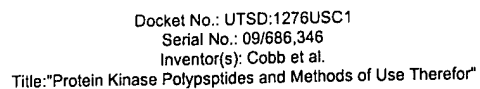
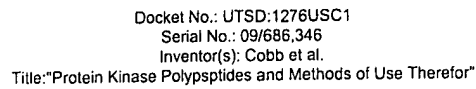


FIG. 18



Query: 526 CTCCAGGGATTACGCTTATTTACATTCTCATACCATGATCCATAGAGATATCAAAGCAGGA 585
|| | ||| | ||| | || | ||| ||| ||| ||| ||| |||
Sbjct: 449 CTGAAGGCCTGGATTATCTGCACTCAGAGCGCAAGATCCACCGAGATATCAAAGTGCC 508

Query: 586 AATATCCTTCTGACAGAACCAGGCCAAGTAAACTTGCTGACTTTGGATGTGCTTCCA 643
|| | ||| | ||| | ||| | ||| ||| ||| ||| |||
Sbjct: 509 AACGTGCTGCTCTCGGAGCAGGGTGATGTGAAGATGGCAGACTTCGGTGTGGCTGGCA 566

FIG. 19A

```

Query:   187  GATCCGGAAAACTCTTCACAGATCTCAGAGAAATCGGCCATGGGAGCTTTGGAGCAGTT  246
          |||||
Sbjct:   119  GACCCAGAGGAACTCTTCACCAAGCTTGACCGCATTGGCAAAGGCTCATTTGGGGAGGTG  178

Query:   247  TATTTTGCACGAGATGTGCGTACTAATGAAGTGGTGGCCATCAAGAAAAT  296
          |||||
Sbjct:   179  TACAAGGGGATCGACAACCACACCAAGGAAGTGGTGGCCATCAAGATCAT  228

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FIG. 19B

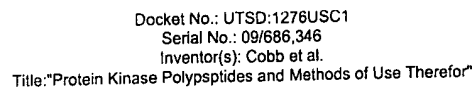


FIG. 20